selecting a mass spectrometer;

selecting a standard compound that forms a non-covalent binding complex with said target molecule, said non-covalent binding complex having a baseline affinity;

mixing an amount of said standard compound with an excess amount of said target molecule such that unbound target molecule is present in said mixture;

introducing said mixture of said standard compound and said target molecule into said mass spectrometer;

adjusting the operating performance conditions of said mass spectrometer such that the signal strength of said standard compound bound to said target molecule is from 1% to about 30% of signal strength of unbound target molecule;

introducing a sub-set of said group of compounds into a test mixture of said target molecule and said standard compound;

introducing said test mixture into said mass spectrometer;

identifying the members of said sub-set that form complexes with said target by discerning signals arising from said members complexed with said target and identifying the members by their respective molecular masses.

31. (amended once) The method of claim 30 wherein said signals are measured as the relative ion abundance.

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34. (amended once) The method of claim 33 wherein said collection library of diverse compounds comprises a historical repository of compounds, a collection of natural products, a collection of drug substances, a collection of intermediates produced in forming drug substances, a collection of dye stuffs, a commercial collection of chemical substances or a combinatorial library of related compounds.

35. (amended once) The method of claim 33 wherein said collection library of diverse compounds comprises a library of compounds having from 2 to about 100,000 members.

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40. (amended once) The method of claim 30 wherein each of the members of said group of compounds, independently, has a molecular mass less than about 200 Daltons,